



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/033,399

DATE: 01/18/2002

TIME: 08:04:15

Input Set : A:\13403.0005NPUS00.ST25.txt

Output Set: N:\CRF3\01182002\J033399.raw

PP-5-4

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Wang, Caili
 4 Zhong, Pingyu
 5 Wang, Xinwei
 7 <120> TITLE OF INVENTION: ADAPTER-DIRECTED DISPLAY SYSTEMS
 9 <130> FILE REFERENCE: 13403.0005NPUS00
 11 <140> CURRENT APPLICATION NUMBER: US/10/033,399
 11 <141> CURRENT FILING DATE: 2001-11-02
 11 <160> NUMBER OF SEQ ID NOS: 24
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 57
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Bacteriophage M13
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 25 <211> LENGTH: 19
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Bacteriophage M13
 29 <400> SEQUENCE: 2
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 49 <211> LENGTH: 222
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: Synthetic, comprising phage gene III leader sequence, GABAB
 recep
 55 tor 2 domain and Myc domain
 57 <400> SEQUENCE: 4
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 62 cagctgcagg acgtcggagg ttgcgcggcc gcagaacaaa aactcatctc agaagaggat 180
 64 ctgagatctg gaggcggtac tgttgaaagt tgtttagcaa aa 222
 67 <210> SEQ ID NO: 5
 68 <211> LENGTH: 74

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69 <212> TYPE: PRT

70 <213> ORGANISM: Artificial Sequence

72 <220> FEATURE:

73 <223> OTHER INFORMATION: Synthetic, comprising phage gene III leader sequence, GABAB
recep

74 tor 2 domain and Myc domain

76 <400> SEQUENCE: 5

78 Leu Val Val Pro Phe Tyr Ser His Ser Ala Thr Ser Arg Leu Glu Gly

79 1 5 10 15

82 Leu Gln Ser Glu Asn His Arg Leu Arg Met Lys Ile Thr Glu Leu Asp

83 20 25 30

86 Lys Asp Leu Glu Glu Val Thr Met Gln Leu Gln Asp Val Gly Gly Cys

87 35 40 45

90 Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Arg Ser Gly

91 50 55 60

94 Gly Gly Thr Val Glu Ser Cys Leu Ala Lys

95 65 70

98 <210> SEQ ID NO: 6

99 <211> LENGTH: 56

100 <212> TYPE: PRT

101 <213> ORGANISM: Artificial Sequence

103 <220> FEATURE:

104 <223> OTHER INFORMATION: Synthetic, comprising phage gene III leader sequence, GABAB
recep

105 tor 2 domain and Myc domain

107 <400> SEQUENCE: 6

109 Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg Leu Arg Met

110 1 5 10 15

113 Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr Met Gln Leu

114 20 25 30

117 Gln Asp Val Gly Gly Cys Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu

118 35 40 45

121 Glu Asp Leu Arg Ser Gly Gly Gly

122 50 55

125 <210> SEQ ID NO: 7

126 <211> LENGTH: 3093

127 <212> TYPE: DNA

128 <213> ORGANISM: Artificial Sequence

130 <220> FEATURE:

131 <223> OTHER INFORMATION: Synthetic, comprising ampicillin gene sequence, ColE1
replication

132 origin, fl replication origin, Plac promoter, GABAB receptor 1 d

133 omain, histidine tag

135 <400> SEQUENCE: 7

136 gcgcaacgca attaatgtga gtagctcac tcattaggca cccagggctt tacactttat 60

138 gcttcggct cgtatgtgt gtggaattgt gagcggataa caatttaccg gttctttaag 120

140 gaggaattaa aaaatgaaat acctattgcc tacggcagcc gctggattgt tattactcgc 180

142 ggcccagccg gccatggcgg ccctgcaggc ctctagagcg gccgctggag gtgaggagaa 240

144 gtcccggctg ttggagaagg agaaccgtga actggaaaag atcattgctg agaaagagga 300

146 gcgtgtctct gaactgcgcc atcaactcca gtctgtagga ggtttagat cttatccata 360

148 cgacgtacca gactacgcag gaggtcatca ccatcatcac cattaatgag tcgacctcga 420

150 ccaattcgcc ctatagttag tcgtattaca attcactggc cgtcgtttta caacgtcgtg 480

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154 gctggcgtaa tagcgaagag gccgcgaccg atcgcccttc ccaacagttg cgcagcctga 600
156 atggcgaaatg ggacgcgccc tgtagcgggc cattaagcgc ggcgggtgtg gtggttacgc 660
158 gcagcgtgac cgctacactt gccagcgccc tagcgccgcg tcctttcgct ttcttccctt 720
160 cctttctcgc caggttcgcc ggctttcccc gtcaagctct aaatcggggg ctccctttag 780
162 ggttccgatt tagtgcttta cggcacctcg accccaaaaa acttgattag ggtgatgggt 840
164 cacgtagtg gcatcgccc tgatagacgg tttttcgccc tttgacgttg gaggccacgt 900
166 tctttaatag tggactcttg ttccaaactg gaacaacact caaccctatc tcggtctatt 960
168 cttttgattt ataagggatt ttgccgattt cggcctattg gttaaaaaat gagctgattt 1020
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172 tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 1140
174 tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa ggaagagtat 1200
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178 ttttctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt tgggtgcacg 1320
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200 cggatcatt gcagcactgg gccagatgg taagccctcc cgtatcgtag ttatctacac 1980
202 gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga taggtgctc 2040
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206 aaaacttcat ttttaattta aaaggatcta ggtgaagatc ctttttgata atctcatgac 2160
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216 ccaccacttc aagaactctg tagcaccgcc tacatactc gctctgctaa tcctgttacc 2460
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230 cgccagcaac gcggcctttt tacggttctt ggccttttgc tggccttttg ctacatggt 2880
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234 taccgtcgc cgacgcgaa cgaccgagc cagcgagtca gtgagcgagg aagcgggaaga 3000
236 gcgccaata cgcaaacgc ctctccccgc gcgttggcg attcattaat gcagctggca 3060
238 cgacaggttt cccgactgga aagcgggcag tga 3093
241 <210> SEQ ID NO: 8
242 <211> LENGTH: 192
243 <212> TYPE: DNA
244 <213> ORGANISM: Bacteriophage M13
246 <400> SEQUENCE: 8

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247 ttagtggtac ctttctattc tcaactccgct taggcttgcg gtggtgcggc cgcagaacaa 60
 249 aaactcatct cagaagagga tctgagatct agatctggag gcggtactgt tgaaagtgt 120
 251 ttagcaaaac ctcatacaga aaattcattt actaacgtct ggaaagacga caaaacttta 180
 253 gatcggttac ct 192

256 <210> SEQ ID NO: 9

257 <211> LENGTH: 64

258 <212> TYPE: PRT

259 <213> ORGANISM: Bacteriophage M13

261 <220> FEATURE:

262 <221> NAME/KEY: MISC_FEATURE

263 <222> LOCATION: (11)..(11)

264 <223> OTHER INFORMATION: Xaa = stop codon

267 <400> SEQUENCE: 9

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 273 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Arg Ser Arg Ser
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 277 Gly Gly Gly Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn
 278 35 40 45
 281 Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala
 282 50 55 60

*Xaa can only represent a single
 amino acid;
 it cannot
 represent a
 stop codon*

285 <210> SEQ ID NO: 10

286 <211> LENGTH: 2962

287 <212> TYPE: DNA

288 <213> ORGANISM: Artificial Sequence

290 <220> FEATURE:

291 <223> OTHER INFORMATION: Synthetic, comprising ampicillin gene sequence, ColE1 replication

292 origin, fl replication origin, Plac promoter, influenza virus he
 293 magglutinin tag

295 <400> SEQUENCE: 10

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 300 cttagtaag gaggaattaa aaaatgaaat acctattgcc tacggcagcc gctggattgt 180
 302 tattactcgc ggcccgaccg gccatggcgg ccctgcaggc ctctagagcg gccgcttacc 240
 304 cgtacgacgt tccggactac gcagggtggct gctgataagt cgacctcgac caattcgccc 300
 306 tatagtgaat cgtattacaa ttcaactggc gtcgtttttac aacgtcgtga ctgggaaaac 360
 308 cctggcggtta cccaacttaa tcgccttgca gcacatcccc ctttcgccag ctggcgtaat 420
 310 agcgaagagg cccgcaccga tcgcctttcc caacagttgc gcagcctgaa tggcggaatgg 480
 312 gacgcgcctt gtacggcgcg attaagcgcg gcgggtgtgg tggttacgcg cagcgtgacc 540
 314 gctacacttg ccagcgccct agcgcgcgct ccttccgctt tcttcccttc ctttctcgcc 600
 316 acgttcgcgc gctttccccc tcaagctcta aatcgggggc tccctttagg gttccgattt 660
 318 agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc acgtagtggg 720
 320 ccacgcacct gatagacggt ttttcgccct ttgacgttgg agtccacgtt ctttaatagt 780
 322 ggactcttgt tccaaactgg aacaacactc aacctatct cggctctatt ttttgattta 840
 324 taaggggatt tgccgatttc ggcctattgg ttaaaaaatg agctgattta acaaaaaatt 900
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338 caatgatgag cactttttaa gttctgctat gtggcgcggt attatcccggt attgacgccc 1320
340 ggcaagagca actcggctgc cgcatacact attctcagaa tgacttggtt gactactcac 1380
342 cagtcacaga aaagcatctt acggatggca tgacagtaag agaattatgc agtgctgcca 1440
344 taaccatgag tgataacact gcggccaaact taacttctgac aacgatcgga ggaccgaagg 1500
346 agctaaccgc ttttttgac aacatggggg atcatgtaac tcgccttgat cgttgggaac 1560
348 cggagctgaa tgaagccata ccaaacgacg agcgtgacac cacgatgcct gtagcaatgg 1620
350 caacaacgtt gcgcaaaacta ttaactggcg aactacttac tctagcttcc cggcaacaat 1680
352 taatagactg gatggaggcg gataaagttg caggaccact tctgcgctcg gcccttccgg 1740
354 ctggctggtt tattgctgat aaatctggag ccggtgagcg tgggtctcgc ggtatcattg 1800
356 cagcactggg gccagatggt aagccctccc gtatcgtagt tatctacacg acggggagtc 1860
358 aggcaactat ggatgaacga aatagacaga tcgctgagat aggtgcctca ctgattaagc 1920
360 attggtaact gtcagaccaa gtttactcat atatacttta gattgattta aaacttcatt 1980
362 tttaatTTAA aaggatctag gtgaagatcc tttttgataa tctcatgacc aaaatccctt 2040
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382 ttccaggggg aaacgcctgg tatctttata gtctgtcgg gtttcgccac ctctgacttg 2640
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386 cggccttttt acggttctcg gccttttctg ggccttttgc tcacatgttc tttctgcgt 2760
388 tatccctga tttctgtgat aaccgtatta ccgcctttga gtgagctgat accgctcgcc 2820
390 gcagccgaac gaccgagcgc agcagtcag tgagcgagga agcggaaagag cgcaccaatac 2880
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394 ccgactggaa agcgggcagt ga
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399 <212> TYPE: DNA
400 <213> ORGANISM: Bacteriophage M13
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405 aaccatcgcc tgcaaatgaa gatcacagag ctggataaag acttggaaga ggtcaccatg 120
407 cagctgcagg acgtcggagg ttgcgcggcc gcagaacaaa aactgatctc agaagaggat 180
409 ctgacgcgtg ctggcggcgg ctctggtggt ggttctggtg gcggtctctga ggggtggcggc 240
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413 ggttccgggt attttgatta tgaaaaaatg gcaaacgcta ataagggggc tatgaccgaa 360
415 aatgccgatg aaaacgcgct acagtctgac gctaaaggca aacttgattc tgcgctact 420
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419 ggtgctactg gtgattttgc tggctctaat tcccaaatgg ctcaagtcgg tgacggtgat 540
421 aattcacctt taatgaataa tttccgtcaa tatttacctt cctcctctca atcggttgaa 600
423 tgtcgccctt ttgtctttgg cgtcggtaaa ccatatgaat tttctattga ttgtgacaaa 660
425 ataaacttat tccgtggtgt ctttgcggtt cttttatatg ttgccacctt tatgtatgta 720
427 ttttctacgt ttgctaacat actgcgtaat aaggagtctt aataaggcgc gccacaattt 780

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to locate a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

MSI →

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14